

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: MEDIGEN SA - c/o LENZ and STAHELIN
(B) STREET: 25 Grand Rue
(C) CITY: GENEVA
(E) COUNTRY: SWITZERLAND
(F) POSTAL CODE (ZIP): CH 1211

(ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF AUTOIMMUNE DISEASE, SUCH AS INSULIN DEPENDENT DIABETES MELLITUS, INVOLVING RETROVIRAL SUPERANTIGENS

(iii) NUMBER OF SEQUENCES: 46

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/EP

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note = "page 11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTTTTGAGTC CCCTTAGTAT TTATT

25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note = "page 26"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCCAACAAC CATGATGGAG

20

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /note= "page 26"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCTCGTAAGG TGCAAATGAA G

21

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii). MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..21
(D) OTHER INFORMATION:/note= "PAGE 26"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTAAAGGATC AAGTGCTGTG C

21

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTTTACAAAG CAGTATTGCT GC

22

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..23
 - (D) OTHER INFORMATION: /note= "RT 1a page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

YAAATGGMGW AYGTYAACAG ACT

23

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..23
 - (D) OTHER INFORMATION: /note= "RT 1b page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

YAAATGGMGW AYGTYAACTG ACT

23

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..28
- (D) OTHER INFORMATION:/note= "RT 2a-nested page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGTCTAGAGC CTCTCCGGCA TGATCCCG

28

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..28
- (D) OTHER INFORMATION:/note= "RT 2b-nested page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGTCTAGAGC CTCTCCGGCA TGATCCCA

28

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..21
- (D) OTHER INFORMATION:/note= "Common 5' anchor page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGC GCCAGCA ATGTATCCAT G

21

00440700-044400

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "SYNTHETIC DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /note = "1K1,2-1 page 50"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGGTGGCAGT GCATCATAGG T

21

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..22
 - (D) OTHER INFORMATION: /note = "4K1,2-4 page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGGAGAGGGT CAGCAGCAGA CA

22

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(D) OTHER INFORMATION: /note= "K1,2-10 page 51"

22

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "synthetic DNA"

(D) OTHER INFORMATION: /note= "K1,2-16 page 51"

19

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "synthetic DNA"

(D) OTHER INFORMATION: /note= "K1,2-17 page 51"

20

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid

(ix) **FEATURE:**

- (D) OTHER INFORMATION:/note= "K1,2-22 page 51"

GGTGTTTCTC CTGAGGGAG

19

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (D) OTHER INFORMATION: /note= "K1,2-26 page 51"

GAAGAATGGC CAACAGAAGC T

21

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..20
- (D) OTHER INFORMATION:/note= "K1,2-27 page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GGGAAACAAG GAGTGTGAGT

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..39
- (D) OTHER INFORMATION:/note= "U3-R-poly(AS) common page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTATATG CGGCCGCTGC GCCAGCAATG TATCCATGG

39

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..21
- (D) OTHER INFORMATION:/note= "RT1 page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TATCTTTCGT TTCTGCAGCA C

21

0044378-09236450

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..22
 - (D) OTHER INFORMATION:/note= "RT2 page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TAACTGGTTG AAGAGCTCGA CC

22

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..21
 - (D) OTHER INFORMATION:/note= "R-U5-1 page 51"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ATACTAAGGG GACTCAGAGG C

21

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(D) OTHER INFORMATION:/note= "R-U5-2 page 51"

CAGAGGCTGG TGGGATCCTC CATATGC

27

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(D) OTHER INFORMATION: /note= "page 52"

TTTTTGAGTC CCCTTAGTAT TTATT

25

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "synthetic DNA"

(D) OTHER INFORMATION:/note= "Page 52"

AGGTATTGTC CAAGGTTTCT CC

22

22

21

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..29
- (D) OTHER INFORMATION:/note= "page 53"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GACTAAGCTT AAGAACCCAT CAGAGATGC

29

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..31
- (D) OTHER INFORMATION:/note= "page 53"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AGACTGGATC CGTTAAGTCG CTATCGACAG C

31

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..208
- (D) OTHER INFORMATION:/note= "FIGURE 7A"

0044270 00406450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCTCCCTC AGGAGAAACA CCCACGAATG ATCAATAAAT ACTAAGGGGA CTCAGAGGCT	60
GGTGGGATCC TCCATATGCT GAACGTTGGT TCCCGGGGCC CCCTTATTTT TTTCTCTATA	120
CTTTGTCTCT GTGTCTTTTT CTTTCCCAAG TCTTCTTCAT TTGCACCTTA CGAGAAACAT	180
CTCCATCATG GTTGTGGAT GGGGGCAA	208

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..1060
- (D) OTHER INFORMATION: /note= "FIGURE 7B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CTGCAGGTGT ACCCAACAGC TCCGAAGAGA CAGTGACATC GAGAACGGGC CATGATGACG	60
ATGGCGGTTT TGTCGAAAAG AAAAGGGGGA AATGTGGGGA AAAGCAAGAG AGATGAGATT	120
GTTACTGTGT CTGTATAGAA AGAAGTAGAC ATAGGAGACT CCATTTTGTT CTGTACTAAG	180
AAAAATTCTT CTGCCTTGAG ATGCTGTAA TCTATGACCT TACCCCAAC CCCGTGCTCT	240
CTGAAACATG TGCCGTGTCA AACTCAGGGT TAAATGGATT AAGGGTGGTG CAAGATGTGC	300
TTTGTTAAAC AGATGCTTGA AGGCAGCATG CTCATTAAGA GTCATCACCA CTCCCTAATC	360
TCAAGTACCC AGGGACACAA AACTGCGAA AGGCCGCAGG GACCTCTGCC TAGGAAAGCC	420
AGGTATTGTC CAAGGTTTCT CCCCATGTGA TAGTCTGAAA TATGGCCTCG TGGGAAGGGA	480
AAGACCTGAC CATCCCCCAG ACCAACACCC GTAAAGGGTC TGTGCTGAGG AGGATTAGTA	540
TAAGAGGAAA GCATGCCTCT TGCAGTTGAG AGAAGAGGAA GACATCTGTC TCCTGCCCAT	600
CCCCTGGGCA ATGGAATGTC TCAGTATAAA ACCCGATTGA ACATTCCATC TACTGAGATA	660
GGGAAAAACT GCCTTAGGGC TGGAGGTGGG ACATGTGGGC AGCAATACTG CTTTGTAAG	720
CATTGAGATG TTTATGTGTA TGTATATCTA AAAGCACAGC ACTTGATCCT TTACCTTGTC	780
TATGATGCAA ACACCTTTGT TCACGTGTTT GTCTGCTGAC CCTCTCCCCA CTATTGTCTT	840
GTGACCCTGA CACATCTCCC TCAGGAGAAA CACCCACGAA TGATCAATAA ATACTAAGGG	900

GA CTCAGAGG CTGGTGGGAT CCTCCATATG CTGAACGTTG GTTCCCGGGG CCCCCTTATT	960
TCTTTCTCTA TACTTTGTCT CTGTGTCTTT TTCTTTTCCA AGTCTTCTTC ATTTGCACCT	1020
TACGAGAAAC ATCTCCATCA TGGTTGTTGG ATGGGGGGCAA	1060

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..1754
- (D) OTHER INFORMATION: /note = "FIGURE 7C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATGGTAACAC CAGTCACATG GATGGATAAT CCTATAGAAG TATATGTTAA TGATAGTGTA	60
TGGGTACCTG GCCCCACAGA TGATCGCTGC CCTGCCAAAC CTGAGGAAGA AGGGATGATG	120
ATAAATATTT CCATTGGGTA TCATTATCCT CCTATTTGCC TAGGGAGAGC ACCAGGATGT	180
TTAATGCCTG CAGTCCAAAA TTGGTTGGTA GAAGTACCTA CTGTCAGTCC TAACAGTAGA	240
TTCAC TTATC ACATGGTAAG CGGGATGTCA CTCAGGCCAC GGGTAAATTA TTTACAAGAC	300
TTTTCTTATC AAAGATCATT AAAATTTAGA CCTAAAGGGA AAAC TTGCC CAAGGAAATT	360
CCTAAAGGAT CAAAGAATAC AGAAGTTTTA GTTTGGGAAG AATGTGTGGC CAATAGTGTG	420
GTGATATTAC AAAACAATGA ATTCGGAAC ATTATAGATT AGGCACCTCG AGGTCAATTC	480
TACCACAATT GCTCAGGACA AACTCAGTCG TGTCCAAGTG CACAAGTGAG TCCAGCTGTC	540
GATAGCGACT TAACAGAAAG TCTAGACAAA CATAAGCATA AAAAATTACA GTCTTTCTAC	600
CTTTGGGAAT GGGAAGAAAA AGGAATCTCT ACCCCAAGAC CAAAAATAAT AAGTCCTGTT	660
TCTGGTCCTG AACATCCAGA ATTGTGGAGG CTTACTGTGG CCTCACACCA CATTAGAATT	720
TGGTCTGGAA ATCAAAC TTT AGAAACAAGA TATCGTAAGC CATTTTATAC TATCGACCTA	780
AATTCCATTC TAACGGTTCC TTTACAAAGT TGCCTAAAGC CCCCTTATAT GCTAGTTGTA	840
GGAAATATAG TTATTAAACC AGCCTCCCAA ACTATAACCT GTGAAAATTG TAGATTGTTT	900
ACTTGCAITG ATTCAACTTT TAATTGGCAG CACCGTATTC TGCTGGTGAG AGCAAGAGAA	960
GGCATGTGGA TCCCTGTGTC CACGGACCGA CCGTGGGAGG CCTCGCCATC CATCCATATT	1020

TTGACTGAAA	TATTAAAAGG	CGTTTTAAAT	AGATCCAAAA	GATTCATTTT	TACTTTAATT	1080
GCAGTGATTA	TGGGATTAAT	TGCAGTCACA	GCTACGGCTG	CTGTGGCAGG	GGTTGCATTG	1140
CACTCTTCTG	TTCAGTCAGT	AAACTTTGTT	AATTATTGGC	AAAAGAATTC	TACAAGATTG	1200
TGGAATTCAC	AATCTAGTAT	TGATCAAAAA	TTGGCAAGTC	AAATTAATGA	TCTTAGACAA	1260
ACTGTCATTT	GGATGGGAGA	CAGGCTTGAC	TTAGAACATC	ATTTCCAGTT	ACAGTGTGAC	1320
TGGAATACGT	CAGATTTTTG	TATTACACCC	CAAATTTATA	ATGAGTCTGA	GCATCACTGG	1380
GACATGGTTA	GACGCCATCT	ACAGGGAAGA	GAAGATAATC	TCACTTTAGA	CATTTCCAAA	1440
TTAAAAGAAC	AAATTTTCGA	AGCATCAAAA	GCCCATTTAA	ATTTGGTGCC	AGGAACTGAG	1500
GCAATTGCAG	GAGTTGCTGA	TGGCCTCGCA	AATCTTAACC	CTGTCACTTG	GATTAAGACC	1560
ATCAGAAGTA	CTATGATTAT	AAATCTCATA	TTAATCGTTG	TGTGCCTGTT	TTGTCTGTTG	1620
TTAGTCTGCA	GGTGTACCCC	AACAGCTCCG	AAAAAAACAG	TGACATCGAG	AACGGGGCCAT	1680
GAATGACAAA	GGCGTTTTTT	GTTCCAAAAA	AAAAAGGGGG	AAATTTTGGG	GAAAACCAAA	1740
AAAATGAAAA	TGTT					1754

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) **FEATURE:**

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..520
(D) OTHER INFORMATION: /note= "FIGURE 7D"

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 59..517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ACATTTGAAG TTCTACAATG AACCCATCAG AGATGCAAAG AAAAGCGCCT CCACGGAG																58
ATG GTA ACA CCA GTC ACA TGG ATG GAT AAT CCT ATA GAA GTA TAT GTT																
Met Val Thr Pro Val Thr Trp Met Asp Asn Pro Ile Glu Val Tyr Val	106															
1 5 10 15																
AAT GAT AGT GTA TGG GTA CCT GGC CCC ACA GAT GAT CGC TGC CCT GCC																
Asn Asp Ser Val Trp Val Pro Gly Pro Thr Asp Asp Arg Cys Pro Ala	154															
20 25 30																

AAA CCT GAG GAA GAA GGG ATG ATG ATA AAT ATT TCC ATT GGG TAT CAT 202
 Lys Pro Glu Glu Glu Gly Met Met Ile Asn Ile Ser Ile Gly Tyr His
 35 40 45
 TAT CCT CCT ATT TGC CTA GGG AGA GCA CCA GGA TGT TTA ATG CCT GCA 250
 Tyr Pro Pro Ile Cys Leu Gly Arg Ala Pro Gly Cys Leu Met Pro Ala
 50 55 60
 GTC CAA AAT TGG TTG GTA GAA GTA CCT ACT GTC AGT CCT AAC AGT AGA 298
 Val Gln Asn Trp Leu Val Glu Val Pro Thr Val Ser Pro Asn Ser Arg
 65 70 75 80
 TTC ACT TAT CAC ATG GTA AGC GGG ATG TCA CTC AGG CCA CGG GTA AAT 346
 Phe Thr Tyr His Met Val Ser Gly Met Ser Leu Arg Pro Arg Val Asn
 85 90 95
 TAT TTA CAA GAC TTT TCT TAT CAA AGA TCA TTA AAA TTT AGA CCT AAA 394
 Tyr Leu Gln Asp Phe Ser Tyr Gln Arg Ser Leu Lys Phe Arg Pro Lys
 100 105 110
 GGG AAA ACT TGC CCC AAG GAA ATT CCT AAA GGA TCA AAG AAT ACA GAA 442
 Gly Lys Thr Cys Pro Lys Glu Ile Pro Lys Gly Ser Lys Asn Thr Glu
 115 120 125
 GTT TTA GTT TGG GAA GAA TGT GTG GCC AAT AGT GTG GTG ATA TTA CAA 490
 Val Leu Val Trp Glu Glu Cys Val Ala Asn Ser Val Val Ile Leu Gln
 130 135 140
 AAC AAT GAA TTC GGA ACT ATT ATA GAT TAG 520
 Asn Asn Glu Phe Gly Thr Ile Ile Asp
 145 150

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Val Thr Pro Val Thr Trp Met Asp Asn Pro Ile Glu Val Tyr Val
 1 5 10 15
 Asn Asp Ser Val Trp Val Pro Gly Pro Thr Asp Asp Arg Cys Pro Ala
 20 25 30
 Lys Pro Glu Glu Glu Gly Met Met Ile Asn Ile Ser Ile Gly Tyr His
 35 40 45
 Tyr Pro Pro Ile Cys Leu Gly Arg Ala Pro Gly Cys Leu Met Pro Ala
 50 55 60
 Val Gln Asn Trp Leu Val Glu Val Pro Thr Val Ser Pro Asn Ser Arg
 65 70 75 80
 Phe Thr Tyr His Met Val Ser Gly Met Ser Leu Arg Pro Arg Val Asn
 85 90 95

Tyr Leu Gln Asp Phe Ser Tyr Gln Arg Ser Leu Lys Phe Arg Pro Lys
100 105 110
Gly Lys Thr Cys Pro Lys Glu Ile Pro Lys Gly Ser Lys Asn Thr Glu
115 120 125
Val Leu Val Trp Glu Glu Cys Val Ala Asn Ser Val Val Ile Leu Gln
130 135 140
Asn Asn Glu Phe Gly Thr Ile Ile Asp
145 150

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "retroviral DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..603
(D) OTHER INFORMATION: /note= "FIGURE 7E"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ACATTTGAAG	TTCTACAATG	AACCCATCAG	AGATGCAAAG	AAAAGCGCCT	CCACGGAGAT	60
GGTAACACCA	GTCACATGGA	TGGATAATCC	TATAGAAGTA	TATGTTAATG	ATAGTGTATG	120
GGTACCTGGC	CCCACAGATG	ATCGCTGCCC	TGCCAAACCT	GAGGAAGAAG	GGATGATGAT	180
AAATATTTCC	ATTGGGTATC	ATTATCCTCC	TATTTGCCTA	GGGAGAGCAC	CAGGATGTTT	240
AATGCCTGCA	GTCCAAAATT	GGTTGGTAGA	AGTACCTACT	GTCACTCCTA	ACAGTAGATT	300
CACTTATCAC	ATGGTAAGCG	GGATGTCACT	CAGGCCACGG	GTAAATTATT	TACAAGACTT	360
TTCTTATCAA	AGATCATTAA	AATTTAGACC	TAAAGGGAAA	ACTTGCCCCA	AGGAAATTCC	420
TAAAGGATCA	AAGAATACAG	AAGTTTTAGT	TTGGGAAGAA	TGTGTGGCCA	ATAGTGTGGT	480
GATATTACAA	AACAATGAAT	TCGGAACTAT	TATAGATTAG	GCACCTCGAG	GTCAATTCTA	540
CCACAATTGC	TCAGGACAAA	CTCAGTCGTG	TCCAAGTGCA	CAAGTGAGTC	CAGCTGTCGA	600
TAG						603

Met	Val	Thr	Pro	Val	Thr	Trp	Met	Asp	Asn	Pro	Ile	Glu	Val	Tyr	Val	1	5	10	15
Asn	Asp	Ser	Val	Trp	Val	Pro	Gly	Pro	Thr	Asp	Asp	Arg	Cys	Pro	Ala	20	25	30	
Lys	Pro	Glu	Glu	Glu	Gly	Met	Met	Ile	Asn	Ile	Ser	Ile	Gly	Tyr	His	35	40	45	
Tyr	Pro	Pro	Ile	Cys	Leu	Gly	Arg	Ala	Pro	Gly	Cys	Leu	Met	Pro	Ala	50	55	60	
Val	Gln	Asn	Trp	Leu	Val	Glu	Val	Pro	Thr	Val	Ser	Pro	Asn	Ser	Arg	65	70	75	80
Phe	Thr	Tyr	His	Met	Val	Ser	Gly	Met	Ser	Leu	Arg	Pro	Arg	Val	Asn	85	90	95	
Tyr	Leu	Gln	Asp	Phe	Ser	Tyr	Gln	Arg	Ser	Leu	Lys	Phe	Arg	Pro	Lys	100	105	110	
Gly	Lys	Thr	Cys	Pro	Lys	Glu	Ile	Pro	Lys	Gly	Ser	Lys	Asn	Thr	Glu	115	120	125	
Val	Leu	Val	Trp	Glu	Glu	Cys	Val	Ala	Asn	Ser	Val	Val	Ile	Leu	Gln	130	135	140	
Asn	Asn	Glu	Phe	Gly	Thr	Ile	Ile	Asp	Glx	Ala	Pro	Arg	Gly	Gln	Phe	145	150	155	160
Tyr	His	Asn	Cys	Ser	Gly	Gln	Thr	Gln	Ser	Cys	Pro	Ser	Ala	Gln	Val	165	170	175	
Ser	Pro	Ala	Val	Asp	Ser	Asp	Leu	Thr	Glu	Ser	Leu	Asp	Lys	His	Lys	180	185	190	
His	Lys	Lys	Leu	Gln	Ser	Phe	Tyr	Leu	Trp	Glu	Trp	Glu	Glu	Lys	Gly	195	200	205	
Ile	Ser	Thr	Pro	Arg	Pro	Lys	Ile	Ile	Ser	Pro	Val	Ser	Gly	Pro	Glu	210	215	220	
His	Pro	Glu	Leu	Trp	Arg	Leu	Thr	Val	Ala	Ser	His	His	Ile	Arg	Ile	225	230	235	240

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..604
- (D) OTHER INFORMATION:/note= "FIGURE 7G"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:59..601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ACATTTGAAG TTCTACAATG AACCCATCAG AGATGCAAAG AAAAGCGCCT CCACGGAG	58
ATG GTA ACA CCA GTC ACA TGG ATG GAT AAT CCT ATA GAA GTA TAT GTT	106
Met Val Thr Pro Val Thr Trp Met Asp Asn Pro Ile Glu Val Tyr Val	
1 5 10 15	
AAT GAT AGT GTA TGG GTA CCT GGC CCC ACA GAT GAT CGC TGC CCT GCC	154
Asn Asp Ser Val Trp Val Pro Gly Pro Thr Asp Asp Arg Cys Pro Ala	
20 25 30	
AAA CCT GAG GAA GAA GGG ATG ATG ATA AAT ATT TCC ATT GGG TAT CAT	202
Lys Pro Glu Glu Glu Gly Met Met Ile Asn Ile Ser Ile Gly Tyr His	
35 40 45	
TAT CCT CCT ATT TGC CTA GGG AGA GCA CCA GGA TGT TTA ATG CCT GCA	250
Tyr Pro Pro Ile Cys Leu Gly Arg Ala Pro Gly Cys Leu Met Pro Ala	
50 55 60	
GTC CAA AAT TGG TTG GTA GAA GTA CCT ACT GTC AGT CCT AAC AGT AGA	298
Val Gln Asn Trp Leu Val Glu Val Pro Thr Val Ser Pro Asn Ser Arg	
65 70 75 80	
TTC ACT TAT CAC ATG GTA AGC GGG ATG TCA CTC AGG CCA CGG GTA AAT	346
Phe Thr Tyr His Met Val Ser Gly Met Ser Leu Arg Pro Arg Val Asn	
85 90 95	
TAT TTA CAA GAC TTT TCT TAT CAA AGA TCA TTA AAA TTT AGA CCT AAA	394
Tyr Leu Gln Asp Phe Ser Tyr Gln Arg Ser Leu Lys Phe Arg Pro Lys	
100 105 110	
GGG AAA ACT TGC CCC AAG GAA ATT CCT AAA GGA TCA AAG AAT ACA GAA	442
Gly Lys Thr Cys Pro Lys Glu Ile Pro Lys Gly Ser Lys Asn Thr Glu	
115 120 125	
GTT TTA GTT TGG GAA GAA TGT GTG GCC AAT AGT GTG GTG ATA TTA CAA	490
Val Leu Val Trp Glu Glu Cys Val Ala Asn Ser Val Val Ile Leu Gln	
130 135 140	

538

586

604

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Glu Ser Ser Cys Arg
180

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

- (A) NAME/KEY: Protein
(B) LOCATION:1..182
(D) OTHER INFORMATION:/note= "FIGURE 7H"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "retroviral DNA"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..250

(D) OTHER INFORMATION: /note= "FIGURE 8A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GTAATGACA CCTATGATGC ACTGCCACCC TTTCACGTGT TCACCCTGAA CATCTGCTTT	60
TTACATCTAA GTGATTGTAC CCAATAAATA GTGTGGAGAC CAGAGCTCTG AGCCTTTTGC	120
AGCCTCCATT TTGCAACTGG TCCCCTGGCT CCCACCTTTA TGAACCTTTA ACCTGTCTTT	180
TCTCATTCCT TTGTACCACAT TGGACTTTGG GTACCCTACG GGTGGTGTG AGGCTGTCAC	240
CGCACATTAA	250

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..203

(D) OTHER INFORMATION: /note= "FIGURE 8B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GTTTAGTTAA TCTATAATCT ATAGAGACAA TGCTTATCAC TGGCTTGCTG TCAATAAATA	60
TGTGGGTAAA TCTCTGTTCA AGACTCTCAG CTTTGAAGCT GTGAGACCCC TGATTTCCCA	120
CTCCACACCT CTATATTTCT GTGTGTGTGT CTTTAATTEC TCCAGTGTG CTGGGTTAGG	180
GTCTCCTCGA CGAGCTGTCG TGC	203

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

004270 00255450

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: /note= "FIGURE 8C"

AACTCAGCTG CTGCACAGTG GTCGAGCCTC CAGAGCTCAT GCCATTGCAG TGGTCAGAGC	60
CTGGCCCTCC TCTTCCTGCA TAGAACCTGG ATTCAATCTG TAAGGTGGGA AGTGCAGCAG	120
CAGAGAACTC TGGCCTTGCA GAGAGTCCCT GTTCCCACTT CACTTTCCTT TTCACCAAAT	180
AAAACCCTGC TTTCACTCAT GCATCAAATT GTCTGTGAGC CTACATTTTT GTGGCCATGG	240
GACAAGAACA CCATCTTTAG CTGAGCTAGG GAAAAGTCCT GCA	283

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 245 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

ii) MOLECULE TYPE: other nucleic acid
  (A) DESCRIPTION: /desc = "retroviral DNA"
```

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: /note= "FIGURE 8D"

GATGTGACCA CTGTGACCTA CCTACACTGG AGATGGCTCA CACTTCCTTA CCCTTCCCCT	60
GCTGTACCAA TAAATAACAG CACAGCCTGA CATTCCGGAGC CATTACCGGT CTTTGTGACT	120
TGGTGGTAGT GGTATCCCCT AGGGCCCAGC TGTCTTTTCT TTTATCTCTT TGTCTTGTGT	180
CTTTATTTCT ATGAGTCTCT CGTCTCCGCA CATGGGGAGA AAAACCCATA GACCCTGTAG	240
GGCTG	245

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

CAGAGAACTC	CAGCCAGCTG	TGATGGAGCC	TCAGGAAGTT	CACAGTTGCA	GCAGGAAGGA	60
GCCTGGCTGC	TCCTCTTCCT	GTGTGGAACC	TGGGATTAGA	ACAGGCTGGC	AGGAAGTGCT	120
TTAGCAGGGA	CTCTGGCCTA	CTCACACTCC	TTGTTTCCCC	CCTTTCTTCC	TTTTCACTCA	180
ATAAAGCCCT	GTCTTACTCA	CCATTCAAAT	TGTCTGTGAG	CCTGAATTTT	CATGGCTGTG	240
GGACAAAGAA	CCCTATTTTT	AGCTGAACTA	AGGAAAATTC	CTGCAA		287

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "RETROVIRAL DNA"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..264
- (D) OTHER INFORMATION: /note= "FIGURE 8G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GTGATTGTCT GCTGACCCTC TCCCCACAAT TGTCTTGTA CCCTGACACA TCCCCCTCTT	60
CGAGAAACAC CCGCGGATGA TCAATAAATA TTAAGGGAAC TCAGAGGCTG GCAGGATCCT	120
CCATATGCTG AACGCTGGTT GCCCCGGGTC CCCTTCTTTC TTTCTCTATA CTTTGTCTCT	180
GTGTCTTTTT CTTTTCCAA TCTCTCGTCC CACCTTACGA GAAACACCCA CAGGTGTGTC	240
CGGGCAACCC AACGCCACAT AACA	264